

AMENDMENTS TO THE SPECIFICATION:

Please replace paragraph [0014] with the following paragraph:

[0014] Structural predictions based on mathematical calculations derived from experimental data such as protein crystal structures (~~Pfam: <http://hits.isb-sib.ch/cgi-bin/PFSCAN>~~) show that all previously known branching enzymes from higher plants have two domains: an alpha-amylase domain and an iso-amylase domain. Here, the iso-amylase domain lies closer to the N-terminus of the protein than the alpha-amylase domain.

Please replace paragraph [000189] with the following paragraph:

[00189] The examination of databases, such as are made available, for example, by EMBL (~~<http://www.ebi.ac.uk/Tools/index.htm>~~) or NCBI (~~National Center for Biotechnology Information, <http://www.ncbi.nlm.nih.gov/>~~), can also be used for identifying homologous sequences, which code for a Class 3 branching enzyme. In this case, one or more sequences are specified as a so-called query. This query sequence is then compared by means of statistical computer programs with sequences, which are contained in the selected databases. Such database queries (e.g. blast or fasta searches) are known to the person skilled in the art and can be carried out by various providers. If such a database query is carried out, e.g. at the NCBI (~~National Center for Biotechnology Information website, <http://www.ncbi.nlm.nih.gov/>~~), then the standard settings, which are specified for the particular comparison inquiry, should be used. For protein sequence comparisons (blastp), these are the following settings: Limit entrez = not activated; Filter = low complexity activated; Expect value = 10; word size = 3; Matrix = BLOSUM62; Gap costs: Existence = 11, Extension = 1.

Please replace paragraph [00206] with the following paragraph:

[00206] In conjunction with the present invention, the term "identity" means a sequence identity over the whole length of the coding region of at least 60%, in particular an identity of at least 70%, preferably greater than 80%, particularly preferably greater than 90% and especially of at least 95%. In conjunction with the present invention, the term "identity" is to be understood to mean the number of amino acids/nucleotides (identity)

corresponding with other proteins/nucleic acids, expressed as a percentage. Identity is preferably determined by comparing the Seq. ID NO 4 or SEQ ID NO 3 with other proteins/nucleic acids with the help of computer programs. If sequences that are compared with one another have different lengths, the identity is to be determined in such a way that the number of amino acids, which have the shorter sequence in common with the longer sequence, determines the percentage quotient of the identity. Preferably, identity is determined by means of the computer program ClustalW, which is well known and available to the public (Thompson et al., Nucleic Acids Research 22 (1994), 4673-4680). ClustalW is made publicly available by Julie Thompson (Thompson@EMBL-Heidelberg.DE) and Toby Gibson (Gibson@EMBL-Heidelberg.DE), European Molecular Biology Laboratory, Meyerhofstrasse 1, D 69117 Heidelberg, Germany. ClustalW can also be downloaded from different Internet sites, including the IGBMC (Institut de Génétique et de Biologie Moléculaire et Cellulaire, B.P.163, 67404 Illkirch Cedex, France; ~~ftp://ftp-igbmc.u-strasbg.fr/pub/~~) and the EBI (~~ftp://ftp.ebi.ac.uk/pub/software/~~) as well as from all mirrored Internet sites of the EBI (European Bioinformatics Institute, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SD, UK).

Please insert the following paragraphs after paragraph [00265]:

Description of the Figures

Table 1 shows the amino acid sequences, contained in the “seed alignment,” that are used for producing the HMM describing for the Pfam isoamylase domain (PF 02922).

Table 2 shows the amino acid sequences, contained in the “seed alignment,” that are used for producing the HMM describing for the Pfam alpha-amylase domain (PF 00128).

Table 3 shows information for producing the HMM for the Pfam isoamylase domain (PF 02922).

Table 4 shows information for producing the HMM for the Pfam alpha-amylase domain (PF 00128).

Please replace the Table number in paragraph [00283] as follows:

[00283] Table 4 A

Please replace paragraph [00289] with the following paragraph:

By sequence comparisons with different branching enzymes, a domain was identified, with the help of which EST databases were examined. In doing so, the EST TC73137 (TIGR database; ~~http://www.tigr.org/tigr-scripts/tgi/te_report.pl?te=TC73137&species=potato~~) from potato was identified.